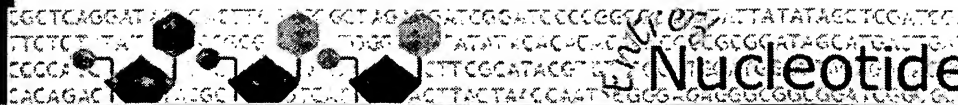


U.S. Serial No. 10/650,108
Amendment Dated 03/16/2005
Reply to Office Action of 12/16/2004



APPENDIX

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PubMed

Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

Books

Search Nucleotide

for mre11

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Details

Field: Gene Name, Limits: Publication Date from 1900/01/01 to 2000/04/18

Display

Summary

Show: 20

Send to

Text

All: 11

bacteria: 0

mRNA: 5

RefSeq: 3



Items 1 - 11 of 11

One page.

☐ 1:

Reports

Links

NM_005590

Homo sapiens MRE11 meiotic recombination 11 homolog A (S. cerevisiae) (MRE11A), transcript variant 2, mRNA
gi|56550106|ref|NM_005590.3|[56550106]

☐ 2:

Reports

Links

NM_005591

Homo sapiens MRE11 meiotic recombination 11 homolog A (S. cerevisiae) (MRE11A), transcript variant 1, mRNA
gi|56550105|ref|NM_005591.3|[56550105]

☐ 3:

Reports

Links

NC_001145

Saccharomyces cerevisiae chromosome XIII, complete chromosome sequence
gi|44829554|ref|NC_001145.2|[44829554]

☐ 4:AE003631 Reports

Links

Drosophila melanogaster chromosome 2L, section 40 of 83 of the complete sequence
gi|55380441|gb|AE003631.4|[55380441]

☐ 5:D11463 Reports

Links

S. cerevisiae MRE11 gene for Mre11 protein, complete cds
gi|1513064|dbj|D11463.1|YSCMRE11[1513064]

☐ 6:AJ243822 Reports

Links

Arabidopsis thaliana mRNA for Mre11 protein (MRE11 gene)
gi|5524768|emb|AJ243822.1|ATH243822[5524768]

☐ 7:AF178433 Reports

Links

Coprinus cinereus DNA repair and meiosis protein Mre11 (mre11) gene, complete cds
gi|5916239|gb|AF178433.1|AF178433[5916239]

About Entrez

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LinkOut

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Related resources
BLAST

Reference sequence project

Search for Genes

Submit to GenBank

Search for full length cDNAs

☐ 8: [AF132144](#) Reports[Links](#)

Drosophila melanogaster clone LD08638 endo/exonuclease Mre11 (mre11) mRNA, complete cds
gi|4928449|gb|AF132144.1|AF132144[4928449]

☐ 9: [AF134569](#) Reports[Links](#)

Xenopus laevis putative nuclease Mre11 (MRE11) mRNA, complete cds
gi|4884903|gb|AF134569.1|AF134569[4884903]

☐ 10: [Z49939](#) Reports[Links](#)

S.cerevisiae chromosome XIII cosmid 9959
gi|887599|emb|Z49939.1|SC9959[887599]

☐ 11: [U60829](#) Reports[Links](#)

Saccharomyces cerevisiae Mre11p (MRE11) gene, complete cds
gi|2209264|gb|U60829.1|SCU60829[2209264]

Display	Summary	Show: 20	Send to	Text
---------	---------	----------	---------	------

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Projects	Analyses	Admin	Alert	SRS	Tutorial
					Help
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Report for **1264_Mre11_sid2 (Protein)**

[Update](#)

Description Case 1264 Mre11 sid2

[Edit](#)

Function **Double-strand break repair protein MRE11.**

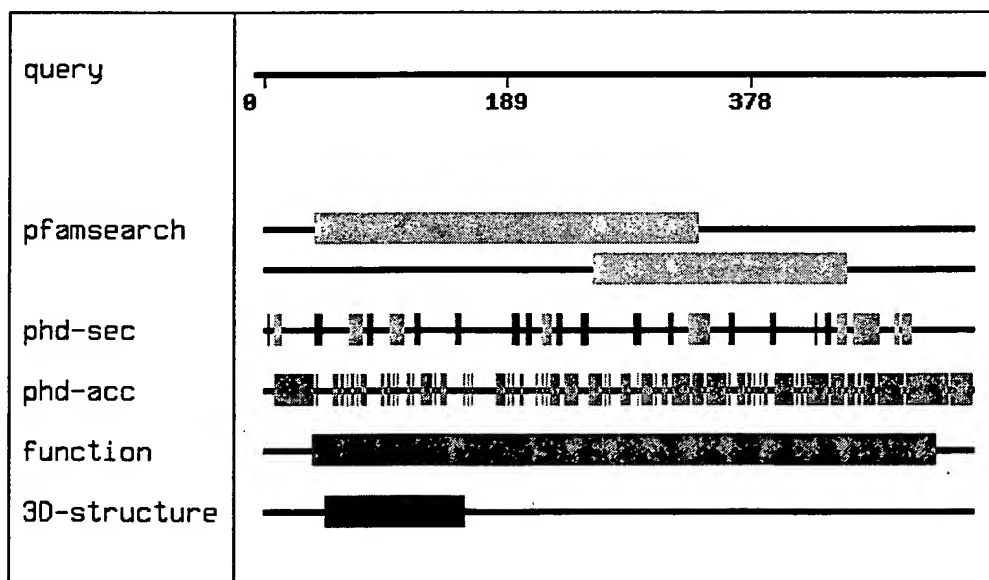
Direct assignment of functionality by identity to
[swissnew|Q9XGM2|MR11_ARATH](#)

in region **39** to **523** for overall length of **720** (87% of query, 67% of hit, [see the alignment](#)).

Functional class Replication

Extracted keywords [Nuclease](#), [Endonuclease](#), [DNA repair](#), [Meiosis](#),
[Hydrolase](#), [Nuclear protein](#), [Exonuclease](#), [Manganese](#)

Features Summary



Homologies

		All BLAST hits
Protein	41 clear homologs	All protein BLAST hits
ESTs	115 homologs	All EST BLAST hits
Patents	37 homologs	All patent hits

Appendix
Part 2

Pramod B. Mahajan
Serial No. 10/650,108

General

Gene name

Molecular weight 61.86 kD

Sequence length 552

Isoelectric point 5.64

Predicted cellular localisation (PHD and PreLoc) [nuclear \(50.5 %\)](#)

Identical sequence segments in: [tr embl|AX287091|AX287091_1](#)
[gp|AX287091|17049072](#)

3D Structure

3D structure inferred by clear homology from residues 48 to 157 in 1II7-A

View [alignment](#)

[pdb|1II7|1II7-A](#) [structure](#)

Phylogeny

Distribution 28 species extracted from 133 [Species](#)
homologous sequences.

Taxa Chordata, Eukaryotae, Fungi,
Planta

Model organisms *Arabidopsis thaliana*,
Caenorhabditis elegans,
Drosophila melanogaster,
Homo sapiens, *Mus musculus*,
Saccharomyces cerevisiae

Features

No significant hits detected by [\[Coils\]](#) [\[Phd-tm\]](#) [\[seg\]](#) biasdb

Patterns

Mre11 DNA-binding presumed domain region from residue **258** to **453**. Source: [\[pfamsearch\]](#) .
Quality: (E=1.9e-85)

Calcineurin-like phosphoesterase region from residue **41** to **338**. Source: [\[pfamsearch\]](#) . Quality:
(E=2.3e-09)

No significant hits found in [\[prositate database\]](#) [\[blocks database\]](#)

Comment

No comment section.

[Edit](#)

Completed Tasks

Start Time

User

Comment

Output

[Interactive](#)

07.03.2003, dressvm
14:04:36

bioSCOUT_default [details...](#)

1

Permissions

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New

Please report problems and feedback concerning bioSCOUT through the [support interface](#).



Alignment: 1264_Mre11_sid2 - pdb|1II7|1II7-A

BLASTP - alignment of 1264_Mre11_sid2 against pdb|1II7|1II7-A

mre11 nuclease

- This hit is scoring at : 3e-06 (expectation value)
- Alignment length (overlap) : 111
- Identities : 32 %
- Scoring matrix : BLOSUM62 (used to infer consensus pattern)
- Database searched : nrdb

```

Q:      48 DCHLGMEKDEIRRFDSF-QAFEEICALADKNKVDFILLGGDLFHENKPSRSTLVKTIEI
      D.HLGY :  : :R :.F :AF:.....A :..VDFIL:.GDLFH.:PS .TL K.I.:
H:      8 DIHLGYEQFHKPQREEEFAEAFKNALEIAVQENVDFILIAGDLFHSSRPSPGTLKKAIAL

      LRRYCLNDQPVKFQVSDQTVNFPNRFKGVNYEDPNFNVGLPVFTIHGNHD      157
      L           Q: :.:.: PVF.I.GNHD
      L-----QIPKEHSI-----PVFAIEGNHD      86
    
```

Legend of Alignment

- : positive score
 - . score between -2 and 0
-

Please report problems and feedback concerning bioSCOUT through the [support interface](#).

HEADER REPLICATION 20-APR-01 1II7
TITLE CRYSTAL STRUCTURE OF P. FURIOSUS MRE11 WITH MANGANESE AND
TITLE 2 DAMP
COMPND MOL_ID: 1;
COMPND 2 MOLECULE: MRE11 NUCLEASE;
COMPND 3 CHAIN: A, B;
COMPND 4 ENGINEERED: YES
SOURCE MOL_ID: 1;
SOURCE 2 ORGANISM_SCIENTIFIC: PYROCOCCUS FURIOSUS;
SOURCE 3 ORGANISM_COMMON: ARCHAEA;
SOURCE 4 EXPRESSION_SYSTEM: ESCHERICHIA COLI;
SOURCE 5 EXPRESSION_SYSTEM_COMMON: BACTERIA
KEYWDS RAD50, MRE11, DNA DOUBLE-STRAND BREAK REPAIR, DAMP,
KEYWDS 2 MANGANESE
EXPDTA X-RAY DIFFRACTION
AUTHOR K.-P.HOPFNER,A.KARCHER,L.CRAIG,T.T.WOO,J.P.CARNEY,J.A.TAINER
REVDAT 1 30-MAY-01 1II7 0
JRNL AUTH K.-P.HOPFNER,A.KARCHER,L.CRAIG,T.T.WOO,J.P.CARNEY,
JRNL AUTH 2 J.A.TAINER
JRNL TITL STRUCTURAL BIOCHEMISTRY AND INTERACTION
JRNL TITL 2 ARCHITECTURE OF THE DNA DOUBLE-STRAND BREAK REPAIR
JRNL TITL 3 MRE11 NUCLEASE AND RAD50 ATPASE
JRNL REF CELL (CAMBRIDGE,MASS.) V. 105 473 2001
JRNL REFN ASTM CELLB5 US ISSN 0092-8674



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				Help	Features

Summary

Searched query 1264_Mre11_sid2 against PFAM database.

Hit	Score	Expect	Description	Q from	Q to	Method
<input type="checkbox"/> pfam hmm Mre11_DNA_bind. alignment	297.3	1.9e-85	Mre11 DNA-binding presumed domain	258	453	HMMPFAM
<input type="checkbox"/> pfam hmm Metallophos. alignment	44.6	2.3e-09	Calcineurin-like phosphoesterase	41	338	HMMPFAM

New Task	Rename Sequences
--------------------------	----------------------------------

Please report problems and feedback concerning bioSCOUT through the [support interface](#).



Alignment: 1264_Mre11_sid2 - pfam|hmm|Mre11_DNA_bind

HMMPFAM - alignment of 1264_Mre11_sid2 against pfam|hmm|Mre11_DNA_bind

Mre11 DNA-binding presumed domain

- This hit is scoring at : 297.3
- Scoring matrix : BLOSUM62 (used to infer consensus pattern)

```

Q: 258 KTNPKSAINEHFL---PGSSVATSLIDGEAKPKHVLLLEIK-GNQYRPTKIPLRSVRPFE
   .:P:. .: F. PGSSVATSL .GEA PKHV LLEIK G.:.: T.IPL::VRPF
H: 1 lIdPeenegkgFyVtQPGSSVATSLspGEAlpKHVgLLeIkYGkkFkltpIPLqTVRPFv

YAEVVLKDEADV----NSNDQDS--VLEHLDK-IVRNLIKSSQ-----PTA-SRS
..E:VL.DE.D: ..ND.D. : :.L : V.:I:.....
mkeiVLadepdilglDrpndtdeRYIqkFLieAkVeemIdeAnaewkekqAdvklgDepr

EPKLPLVRIKVDYSG-----FSTINPQRFQKYGKQVANPQDILIFSKSAKKRQTG
:P.LPL:R::VDY:G :.T.NP RFGQ::VG:VANP.D:: F.K..K:.....
qPpLPLIRLrVDYtggnqtqdwldyqtFNpiRFgqrFvGrVANpnDvvqFkkkkKpkekka

D-----HIDDSEKL RPEELNQQTIEALV-----AESNLKMEILPVDDLDIALHD
: . D.E L..E:LN. :.E.LV AE.N :.:LP .L. A:..
nteveiNftkllddrdeellaseklalnrlVetLVneYletAeknkqLslLperglgeAvqe

F 453
F
F 241
    
```

Legend of Alignment

- : positive score
- . score between -2 and 0

Please report problems and feedback concerning bioSCOUT through the [support interface](#).



Alignment: 1264 Mre11 sid2 - pfam|hmm|Metallophos

HMMPFAM - alignment of 1264 Mre11 sid2 against pfam|hmm|Metallophos

Calcineurin-like phosphoesterase

- This hit is scoring at : 44.6
- Scoring matrix : BLOSUM62 (used to infer consensus pattern)

```

Q:      41 LRILVATDCHLGYMEKdeirrfsfqafEEICALAdKnKVDFILLGGDLFHENKPSRSTL
      :RILV. D.H G: :                               :...LA : K D.:L. GDL....PS ..L
H:      1 mrilvigDlHggfedl.....llllela.e.kpdlvflGDlvdrpgpslevl

      VKTieilrrycldqpvkfqvvsdqtvnfpnrfgkvnyEDPNFNVGLPVFTIHGNHDDPA
      : .                                           .... PV:...GNHD :
      lll.....falklkapgpvyivrGNHDFds

      GVDNLsaidilsacnlvnyfgkmdlgsgvgqiavypvlvkkgmtsvalyglgnirderl
      G . .
      gnsvy.....

      nrmfqtphSVQWMPGtQDGESaSDWFNlVLHQNRlKtNpksainehflpgssvatsli
      :... : .IL::H . ..
      .....welfleef.lllla.lvdgkillvHgglsdp.....

      dgeakpkhvlleikgnqyrptkiplrsvrpfeyaevvlkDEADVNSNDQDSVL---EHl
      E. :. N. D V: .H
      .....leellk.ngvdlvirGHtH.

      D      338
      .
      p      124

```

Legend of Alignment

```
: positive score
```

. score between -2 and 0

Please report problems and feedback concerning bioSCOUT through the [support interface](#).

```
!!AA_MULTIPLE_ALIGNMENT 1.0
FileUp of: @/tmp/47563335.list
```

Symbol comparison table: genrundata:blosum62.cmp CompCheck: 1102

GapWeight: 8 GapLengthWeight: 2

```
1264AB010695_pileup_47563.txt  MSF: 805  Type: P  March 13, 2003 16:53  Check:
7228 ..
```

U37359aa Human Mre11 protein encoded by GenBank U37359
U58987aa Mouse Mre11 protein encoded by GenBank U58987
AB010695aa Arabidopsis Mre11 protein encoded by GenBank AB010695
AJ243822aa Arabidopsis Mre11 protein encoded by GenBank AJ243822
1264sid2 Case 1264 Mre11 SEQ ID NO: 2
D11463aa S. cerevisiae Mre11 protein encoded by GenBank D11463
X82322 S. pombe Rad32 protein encoded by GenBank X82322

Identical to 1264sid2

* Conserved Asp required for nuclease activity (Example 4)

Underlined phosphodiesterase/nuclease motifs (Example 4)

Double-underlined Pfam MRE11 DNA bind domain (Quality E=1.9e-85)

Italicized Pfam Metallophos domain (Quality E=2.3e-09)

[illegible]

51 100

AB010695aa LGYMEKDEIR RHDSEKATEE IG AAEKQV DE ILCCDLF HENKPSR TL

AJ243822aa LGYMEKDEIR RHDSEKATEE IG AAEKQV DE ILCCDLF HENKPSR TL

1264sid2 LGYMEKDEIR RHDSEKATEE IG AAEKQV DE ILCCDLF HENKPSR TL Motif

U37359aa LG MEKDAAR GNDIEV L E ILRLAQENEV DFILCCDLF HENKPSRKTIL

U58987aa LG MEKDA R GNDIEV F E ILRLALENEV DFILCCDLF HENKPSRKTIL

D11463aa GYNENDPIT GDDS KLEHE MMLAKNNNV DM QSCDLF HVNKPS KIL

X82322aa GYGEKDP R GNDSEV LNE HLE ARERDV DMILCCD F H NKPSRKIL

101 150

AB010695aa VK IETLRRH CLNDKEVQEQ VVSDQTVNEQ .NAFCQVNYE DEHENVGLPV

AJ243822aa VK IETLRRH CLNDKEVQEQ VVSDQTVNEQ .NAFCQVNYE DEHENVGLPV

1264sid2 VK IETLRRH CLNDKEVQEQ VVSDQTVNEQ .NAFCQVNYE DEHENVGLPV

U37359aa HTC E LR Y C GDERVQFE V SDO VNEG FS EPWVNYQ DGNLNI S EV

U58987aa HSC E LR Y C GDERVQFE V SDO VNEG FS EPWVNYQ DGNLNI S EV

D11463aa YQV KTLRLC C GDKICELE V SDP QVEH YDEFTNVNYE DPNFN S EV

X82322aa YQ RSLRLN CLGDKICELE V SDT TTG DTAVCN NYL DPNINVA EV

	151		200
AB010695aa	E I HGNHDDP AGVDNL SAID ILSACNLVNY FGK MVLGGSG VGOI YPFI		
AJ243822aa	E I HGNHDDP AGVDNL SAID ILSACNLVNY FGK MVLGGSG VGOI YPFI		
1264sid2	E I HGNHDDP AGVDNL SAID ILSACNLVNY FGK MVLGGSG VGOI YPFI		Motif
U37359aa	E I HGNHDDP GADALCAID ILSACG FVNH FG SM....S VEKID SPVL		
U58987aa	E I HGNHDDP GADALCAID ILSACG FVNH FG SM....S VEKID SPVL		
D11463aa	EGLSGNHDDA GDSL LCPD L L HATGLNH FGK I....E SDKIKVVPFI		
X82322aa	E I HGNHDDP GDGRYSAID L L QVTGLVNY FG P....E ND L I VVSPFI		

	201		250
AB010695aa	KKGST VAL YGLGNIRDER LNRMFOTPH VQWMRHEVO GCDVSDWFTI		
AJ243822aa	KKGST VAL YGLGNIRDER LNRMFOTPH VQWMRHEVO GCDVSDWFTI		
1264sid2	KKGST VAL YGLGNIRDER LNRMFOTPH VQWMRHEVO GCDVSDWFTI		
U37359aa	QKGSTK AL YGLGSTPDER IYRMFVN.KK VTM RHEKED N....SWFTI		
U58987aa	QKGSTK AL YGLGSTPDER IYRMFVN.KK VTM RHEKED N....SWFTI		
D11463aa	FQKGSTK AL YGLAA RDER LFRTEKD.GG VTFEVETMR G....SWFTI		
X82322aa	QKGSTK AL YG SN RDER LYHSEFE.NK VK R E DLYR D....SWFTI		

	251		300
AB010695aa	LVLHONR K NPKNAISEHF IPRFLDFIVW GHEHECLIDP QEVSGMGFHI		
AJ243822aa	LVLHONR K NPKNAISEHF IPRFLDFIVW GHEHECLIDP QEVSGMGFHI		
1264sid2	LVLHONR K NPKNAISEHF IPRFLDFIVW GHEHECLIDP QEVSGMGFHI		
U37359aa	FVLHONRSKH GSTNFIPEQF LDDFIDLVIW GHEHECKIAP TKNEQQLFYI		
U58987aa	FVLHONRSKH GNTNFIPEQF LDDFIDLVIW GHEHECKIGP IKNEQQLFYI		
D11463aa	YCHONHTGH TNT FPEQF LPDFLDMVIW GHEHECIPNL VHNPIKNFDV		
X82322aa	LT HONHSAH TETSY PESE LQDFYDFVLW GHEHECLIDG SYNPTQKFTV		

	301		350
AB010695aa	TQPGSSVATS LIDGESKPKH VLLLEIK.GN QYRPTKIPIT SVRPFEEYIE		
AJ243822aa	TQPGSSVATS LIDGESKPKH VLLLEIK.GN QYRPTKIPIT SVRPFEEYIE		
1264sid2	..PGSSVATS LIDGEAKPKH VLLLEIK.GN QYRPTKIPLR SVRPFEEYIE		Mrel1_DNA
U37359aa	SQPGSSVATS LSPGEAVKKH VGLLRIK.GR KMNMHKIPIH VRQFME		
U58987aa	SQPGSSVATS LSPGEAVKKH VGLLRIK.GR KMNMOX PLR VRREFIE V		
D11463aa	LQPGSSVATS LC AEAOPKY MF L L KYCE AP MFIPIE RTKMKKS		
X82322aa	VQPGS ATS LSPGE AKKH CG LINTT.GK D HLEKIRLR VRPHIMK		

	351		400
AB010695aa	VLKDE D DP NDQNS LEHLDK VRN..... LIEK SKK		
AJ243822aa	VLKDE D DP NDQNS LEHLDK VRN..... LIEK SKK		
1264sid2	VLKDE D NS NDQDSV LEHLDK VRN..... LIEKSKQ		
U37359aa	VLANHPD FN PD PKMTQAI QSFCLEK E ENAERE.. R		
U58987aa	VLANHPN FN PD PKMTQAI QSFCLEK E DSAERE.. R		
D11463aa	SLQDVPH RP ..HDK..DAT SKYL EO E RDANEETK QKTA DGEGD		
X82322aa	ELSVS PP MVENK..KEV LTYL SK E A TEANAQWY EA...QGIVE		

	401		450
AB010695aa	VNRSEIKLP LVRIKVDYSGF MTINPQREGQ KYVGKVANPQ		
AJ243822aa	VNRSEIKLP LVRIKVDYSGF MTINPQREGQ KYVGKVANPQ		
1264sid2	VNRSEIKLP LVRIKVDYSGF MTINPQREGQ KYVGKVANPQ		
U37359aa	LGNSHQEKP LVR VDYSGGE EPFSVLRESQ KMD VANHK		
U58987aa	LGNPQOEKP L R VDYSGGE EPFVLRRESQ KMD VANHK		
D11463aa	MV...ELPK L R VDYSA PSNTQSPID QVENPRES QK VG VANG		
X82322aa	VVENKEPLP L R VDY GG QVENPQRES K VG VANAT		

	451		500
AB010695aa	DILLIE....S K K KGR EA .N...IDDSE	LRE...EELN OONTFAIV..	
AJ243822aa	DILLIE....S K K KGR EA .N...IDDSE	LRE...EELN OONTFAIV..	
1264sid2	DILLIE....S K K KGR EA .N...IDDSE	LRE...EELN OONTFAIV..	
U37359aa	DH HFRHRE Q..E TGE E INFGK.... IT E.SE.GT TLR EDLVKQ		
U58987aa	DH HFRHRE Q..E TGE E INFGM.... IT EASE.GA TLR EDLVKQ		
D11463aa	N OFYKKRS PV S K E INGTSSSR VE LFS SGG ELE Q LVND		
X82322aa	D OFYLKKK .Y S SRNDG LYTSA EDIK I.....N SLR E LVNE		

	501		550
AB010695aaAESNLK MEILPVDLD	ALHNEVNKD DK AFYSC Q	YNIQETFGKI
AJ243822aaAESNLK MEILPVDLD	ALHNEVNKD DK AFYSC Q	YNIQETFGKI
1264sid2AESNLK MEILPVDLD	ALHNEVNKD DK AFYSC Q	YNIQETFGKI
U37359aa	YFQTAEKN Q S LTERG G EA Q EVDK	KDAIEEL K Y LEKIQRFI	
U58987aa	YFQTAEKN Q S LTERG G EA Q EVDK	KDAIEEL K Y LEKIQRFI	
D11463aa	LL....NK Q S LEEVGN EA KKEVDK	KTALKEF S HEI SNEVGIL	
X82322aa	YL....KTN ECLFEDSLG EA VNEVEKD D DAIKE~~~	~~~~~	

	551		600
AB010695aa	K DAKKE E D I KVGE C EER K RSR.P	IGSS....
AJ243822aa	K DAKKE E D I KVGE C EER K RSR.P	IGSS....
1264sid2	S DAKKE E D I KVGE C EER K RS	LHSK GRLT	IGSHNLVF
U37359aa	KERHID LE KIDEEV RFR ETRO NTNEE DDEVRE MTR	R LRSQSEE	
U58987aa	KERHID LE KIDEEV RFR ESRQ NTNEE DDEVRE MSR	R LRSQSET	
D11463aa	S NEFL T A E KALIK Q KRANSVP	TPPK NDET N	FAFNGNGLDS
X82322aa	~~~~~	~~~~~	~~~~~

	601		650
AB010695aa	LSTG TSEN TKCS CIANA SFC DDEDTTQ	MSGLAPPTRG	RRGSSTANTT
AJ243822aa	LSTG TSEN TKCS CIANA SFC DDEDTTQ	MSGLAPPTRG	RRGSSTANTT
1264sid2	LSLN FSFC FPG CYWLA SNSYN	~~~~~	~~~~~
U37359aa	S SAFS DD MSIDLAEQM NDS DDISAA	TNKG RGRGRG	RRGGRQNSA
U58987aa	S SAFS ED .SFD SEQTA NDS DDSL SAV	PSRGRGRGRG	RRGARGQSSA
D11463aa	FRSSNREVRT GSPDITQSHV D NESR THIS	QAESSKPTSK	PKRVRTATKK
X82322aa	~~~~~	~~~~~	~~~~~

	651		700
AB010695aa	RGRAKAPTRG RGRGKASSAM KQTTLDSSLG	FRQSQRSASA	AASAAFKSAS
AJ243822aa	RGRAKAPTRG RGRGKASSAM KQTTLDSSLG	FRQSQRSASA	AASAAFKSAS
1264sid2	~~~~~	~~~~~	~~~~~
U37359aa	SRGGSQRGR.AFKS	TRQQPSRNV T
U58987aa	PRGGSQRGRD TGLEITTRGR SSKATSSTSR	NMSIIDAFRS	TRQQPSRNV A
D11463aa	KIPAFSDSTV ISDAENELGD NDAQDDVDI	DENDIIMVST	DEEDASYGLL
X82322aa	~~~~~	~~~~~	~~~~~

	701		750
AB010695aa	TIGEDDVDSP SSEEVEPEDF NKP DSS EDD	ESTKGKGRKR	PATTKRGRGR
AJ243822aa	TIGEDDVDSP SSEEVEPEDF NKP DSS EDD	ESTKGKGRKR	PATTKRGRGR
1264sid2	~~~~~	~~~~~	~~~~~
U37359aa	TKNYSEVIEV DESDVEEDIF PTTSKTDQRW	SSTSSSKIMS	QSQVSKGVDF
U58987aa	PKNYSETIEV DDS D EDDIF PTNSRADQRW	SGTTSSKRMS	QSQTAKGVDF
D11463aa	NGRKTKTKTR PAASTKTASR RGKGRAS RTP	KTDILGSLLA	KKRK~~~~~
X82322aa	~~~~~	~~~~~	~~~~~

	751				800
AB010695aa	GSGTSKRGRK	NESSSSLNRL	LSSKDDDEDE	DDEDREKKLN	KSQPRVTRNY
AJ243822aa	GSGTSKRGRK	NESSSSLNRL	LSSKDDDEDE	DDEDREKKLN	KSQPRVTRNY
1264sid2	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
U37359aa	ESSEDDDDDP	FMNTSSLRRN	RR~~~~~	~~~~~	~~~~~
U58987aa	ESDEDDDDDP	FMSSSCPRRN	RR~~~~~	~~~~~	~~~~~
D11463aa	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
X82322aa	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~

	801
AB010695aa	GALRR
AJ243822aa	GALRR
1264sid2	~~~~~
U37359aa	~~~~~
U58987aa	~~~~~
D11463aa	~~~~~
X82322aa	~~~~~



Mre11_DNA_bind

Accession number: PF04152

Previous identifiers: Mre11_DNA_bind;

Mre11 DNA-binding presumed domain[Add/Annotation](#)

The Mre11 complex is a multi-subunit nuclease that is composed of Mre11, Rad50 and Nbs1/Xrs2, and is involved in checkpoint signalling and DNA replication [1]. Mre11 has an intrinsic DNA-binding activity that is stimulated by Rad50 on its own or in combination with Nbs1 [2].

INTERPRO description (entry IPR007281)

The Mre11 complex is a multi-subunit nuclease that is composed of Mre11, Rad50 and Nbs1/Xrs2, and is involved in checkpoint signalling and DNA replication MEDLINE:11988766. Mre11 has an intrinsic DNA-binding activity that is stimulated by Rad50 on its own or in combination with Nbs1 MEDLINE:10823903.

QuickGO**FUNCTION :**

manganese ion binding (GO:0030145)

PROCESS :

double-strand break repair (GO:0006302)

COMPONENT :

nucleus (GO:0005634)

Alignment
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 ☐ Full (31)
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Species Distribution**Domain organisation**

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☐ View architectures for 31 proteins

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NEW! View alignments & domain organisation by species Tree depth : Show all levels View Species Tree	Download tree ATV Applet The trees were generated using Quicktree To find out more about ATV phylogenetic tree-viewer click here

Database References

SYSTERS	Mre11_DNA_bind
PANDIT	Mre11_DNA_bind
FUNSHIFT	Mre11_DNA_bind

Literature References

1.
A mechanistic basis for Mre11-directed DNA joining at microhomologies.
 Paull TT, Gellert M;
 Proc Natl Acad Sci U S A 2000;97:6409-6414.

2.
The Mre11 complex: at the crossroads of dna repair and checkpoint signalling.
 D'Amours D, Jackson SP;
 Nat Rev Mol Cell Biol 2002;3:317-327.

Pfam specific information

Author of entry	Wood V, Finn RD
Type definition	Domain
Source of seed members	Pfam-B_3909 (release 7.3);
Average Length	201.4
Average %id	37
Average Coverage	28.62%

HMMER build information

	Pfam_ls [Download HMM]	Pfam_fs [Download HMM]
Gathering cutoff	25.0 25.0;	25.0 25.0
Trusted cutoff	71.9 71.9;	49.5 32.0
Noise cutoff	13.1 13.1;	8.2 17.4
Build method of HMM	hmmbuild -F HMM_ls SEED hmmcalibrate --seed 0 HMM_ls	hmmbuild -f -F HMM_fs SEED hmmcalibrate --seed 0 HMM_fs

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Metallophos



Figure 1: 1hpu Hydrolase

5'-nucleotidase (closed form), complex with ampcp

Key:

Domain	Chain	Start Residue	End Residue
Metallophos	A	34	256
5'-nucleotid C	A	363	511
Metallophos	B	34	256
5'-nucleotid C	B	363	511
Metallophos	C	34	256
5'-nucleotid C	C	363	511
Metallophos	D	34	256
5'-nucleotid C	D	363	511

The Swissprot/PDB mapping was provided by MSD

1aui

Display pdb

Alignment

Accession number: PF00149

Previous identifiers: STphosphatase;

Calcineurin-like phosphoesterase[Add Annotation](#)

This family includes a diverse range of phosphoesterases [1], including protein phosphoserine phosphatases, nucleotidases, sphingomyelin phosphodiesterases and 2'-3' cAMP phosphodiesterases as well as nucleases such as bacterial SbcD [SBCD_ECOLI](#) or yeast MRE11 [MR11_YEAST](#). The most conserved regions in this superfamily centre around the metal chelating residues.

KEY! This family forms **interactions** with other Pfam families, to view them click [here](#)

INTERPRO description (entry IPR004843)

Protein phosphorylation plays a central role in the regulation of cell functions [MEDLINE:2827745](#), causing the activation or inhibition of many enzymes involved in various biochemical pathways [MEDLINE:2176161](#). Kinases and phosphatases are the enzymes responsible for this, and may themselves be subject to control through the action of hormones and growth factors [MEDLINE:2827745](#). Serine/threonine (S/T) phosphatases catalyse the dephosphorylation of phosphoserine and phosphothreonine residues. In mammalian tissues four different types of PP have been identified and are known as PP1, PP2A, PP2B and PP2C. Except for PP2C, these enzymes are evolutionary related. The catalytic regions of the proteins are well conserved and have a slow mutation rate, suggesting that major changes in these regions are highly detrimental [MEDLINE:2827745](#).

The metallo-phosphoesterase motif is found in a large number of proteins involved in phosphorylation. These include serine/threonine phosphatases, DNA polymerase, exonucleases, and other phosphatases.

QuickGO**FUNCTION :**hydrolase activity ([GO:0016787](#))**Domain organisation**

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Database References			
PDB You can find out how to set up Rasmol here		1g5b A; 13; 190; <div> <div>PDB 2 Pfam</div> <div>Scop Cath Pfam</div> <div>Rasmol Chime Jmol</div> <div>PDBSUM SCOP-UK MSD</div> </div>	
COGS		COG0420 COG0622 COG0639 COG0737 COG1311 COG1407 COG1408 COG1409 COG1692 COG1768 COG2129 COG2908	
HOMSTRAD		stpb	
PFAMB		PB138897 PB138852 PB138821 PB138819 PB138082 PB137993 PB137778 PB137151 PB136893 PB136624 PB136447 PB136110 PB135893 PB135664 PB135104 PB134487 PB134107 PB133997 PB133801 PB133587 PB129622 PB121941 PB109640 PB095241 PB075242 PB065007 PB061303 PB051159 PB047522 PB046470 PB029770 PB022149 PB012730 PB001928	
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Pfam specific information

1.
Phosphoesterase domains
associated with DNA polymerases
of diverse origins.

Aravind L, Koonin EV;
 Nucleic Acids Res 1998;26:3746-3752.

Author of entry	Diakic M
Type definition	Domain
Source of seed member s	Diakic M
Average Length	195.5
Average %id	15
Average Coverage	50.41%

HMMER build information

	Pfam_ls [Download HMM]	Pfam_fs [Download HMM]
Gathering cutoff	22.0 22.0;	14.0 14.0
Trusted cutoff	22.2 22.2;	14.0 14.0
Noise cutoff	21.9 21.9;	13.9 13.9
Build method of HMM	hmmbuild -F HMM_ls SEED hmmcalibrate --seed 0 HMM_ls	hmmbuild -f -F HMM_fs SEED hmmcalibrate --seed 0 HMM_fs

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Replication
PDB Id
1ii7

PDB Id: 1ii7

Name: Replication

Title: Crystal structure of p. Furiosus mre11 with manganese and damp

Structure: Mre11 nuclease. Chain: a, b. Engineered: yes

Source: Pyrococcus furiosus. Archaea. Expressed in: escherichia coli.

UniProt: Q8U1N9 (Q8U1N9) [Pfam]

Function: (see GO annotation below)

Resolution: 2.20Å

R-factor: 0.222

R-free: 0.264

Authors: K.-P.Hopfner, A.Karcher, L.Craig, T.T.Woo, J.P. Carney, J.A.Tainer

Date: 20-Apr-01

Related entries: 1ii8

1f2t

1f2u

Gene Ontology (GO) functional annotation



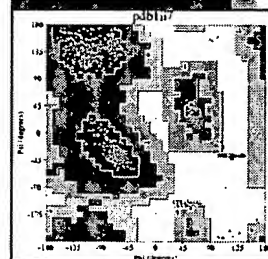
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Biochemical function	hydrolase activity	5 term (s)

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Clefts



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Protein chains

A B 333 a.a. *

Ligands

PO4

SO4 x3

101

Metal ions

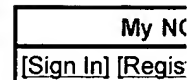
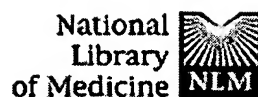
_MN x4

Waters x 264

* Residue conservation analysis

 Go to PDB
code:

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1: Cell. 2001 May 18;105(4):473-85.

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Cell Press

Structural biochemistry and interaction architecture of the DNA double-strand break repair Mre11 nuclease and Rad50-ATPase

Hopfner KP, Karcher A, Craig L, Woo TT, Carney JP, Tainer JA.

Department of Molecular Biology and Skaggs Institute for Chemical Biology, The Scripps Research Institute, La Jolla, CA 92037, USA.

To clarify functions of the Mre11/Rad50 (MR) complex in DNA double-strand break repair, we report *Pyrococcus furiosus* Mre11 crystal structures, revealing a protein phosphatase-like, dimanganese binding domain capped by a unique domain controlling active site access. The structures unify Mre11's multiple nuclease activities in a single endo/exonuclease mechanism and reveal eukaryotic macromolecular interaction sites by mapping human and yeast Mre11 mutations. Furthermore, the structure of the *P. furiosus* Rad50 ABC-ATPase with adjacent coiled-coil defines a compact Mre11/Rad50-ATPase complex and suggests that Rad50-ATP-driven conformational switching directly controls the Mre11 exonuclease. Electron microscopy, small angle X-ray scattering, and ultracentrifugation data of human and *P. furiosus* MR

reveal a dual functional complex consisting of a (Mre11)2/(Rad50)2 heterotetrameric DNA processing head and a double coiled-coil linker

PMID: 11371344 [PubMed - indexed for MEDLINE]

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